

GetPage version 1.1  
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Run on: January 12, 2003, 07:11:12  
 Target: 44462439  
 Count: 1000000000

(without alignments)  
16472 499 Million 2011 - 2012/2013

Title: US-09-864-711-1

SID  
10-1

Scoring table: IDENTITY AND

[illegible][illegible]

maximum DB seq length: 0

Post-processing: Minimum Match: 0%

Listing 4: 45

உதவி

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41: em_hrg_vt.*

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score greater than or equal to the score of the resident being interviewed. The difference between the two scores was calculated.

## SUMMARIES

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1	194.4	98.4	217	6	AB444210	AB444210 Sequence
2	171.6	97.1	183	6	AB011457	AB011457 Sequence
3	149.6	92.8	220	2	AF020935	AF020935 Homo sapi
4	137.6	90.6	229	0	AF020147	AF020147 Homo sapi
5	1168.4	59.4	2046	10	AF016170	AF016170 Homo sapi
6	111.6	97.8	173	2	AF016170	AF016170 Homo sapi
7	644	92.8	857	3	AB022935	AB022935 Homo sapi
8	453.4	93.1	123	6	AB011457	AB011457 Sequence
9	440	92.8	123	6	AB011457	AB011457 Sequence
10	345.6	91.5	434	1	G37224	G37224 Homo sapi
11	324.6	91.1	327	1	AB011457	AB011457 Sequence
12	200.6	107.2	27191	2	AF010895	AF010895 MS muscu
13	184.4	94.4	414	1	AB011457	AB011457 Sequence
14	164.6	8.4	444	10	AB022681	AB022681 Homo sapi
15	164.6	8.4	460	6	122544	122544 Sequence
16	125	7.5	167	6	AB044147	AB044147 Sequence
17	164	7.8	198494	9	AC033585	AC033585 Homo sapi
18	137	7.6	5129	4	AF034312	AF034312 Sequence
19	130.2	6.6	12241	2	AC012292	AC012292 Sequence
20	128.6	6.6	1294	10	AB011457	AB011457 Sequence
21	128.6	6.5	6552	10	MM031436	MM031436 Homo sapi
22	104.4	6.3	7593	9	HS024212	HS024212 Homo sapi
23	104.4	6.3	7593	9	HS024212	HS024212 Homo sapi
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37	58.4	3.0	1112	4	AB022935	AB022935 Homo sapi
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## ATTACHMENTS

Fred. No. is the number of results predicted by chance to have a

[illegible]

















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 11 436 TTGAAAGAACTTGGCTTATTTGGCAAGTGTGTGGCTGTG 538  
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 CHEMICAL N sequence 7 from Parent W00110902.  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;  
 Hominidae; Homo sapiens  
 1 (bases 1 to 1653)  
 SHANKS R.A. and Fernandes E.  
 Nucleic acids and encoded polypeptides encoded thereby  
 Patent: WO 0110902-A 7 15-FEB-2001;  
 CANADA  
 Canadian Corporation (US)  
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BASE COUNT 436 A 421 C 383 G 423 T  
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 Best Local Similarity 99.93; Pred. No. 40-997  
 Mismatch 0; Mismatches 0; Indels 1; Gaps 1;

37 1653 TAAAGTAAAGTATTAAGAAAGTATTAAGAAAGTATTAAGAAAGTATTAAGTGG 60  
 11 1653 TAAAGTAAAGTATTAAGAAAGTATTAAGAAAGTATTAAGTGG 1019  
 37 1653 TAAAGTAAAGTATTAAGAAAGTATTAAGAAAGTATTAAGTGG 119  
 11 1653 TAAAGTAAAGTATTAAGAAAGTATTAAGAAAGTATTAAGTGG 1079  
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 11 1653 TAAAGTAAAGTATTAAGAAAGTATTAAGAAAGTATTAAGTGG 1319  
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## RESULT 10

G37224/2

LOCUS

DEFINITION

ACCESSION

VERSION

FEATURES

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

COMMENT

G37224  
 SH9C-57224 Human Homo sapiens STS genomic, sequence (aired) file.  
 G37224  
 G37224.1 G112996879  
 STS  
 Homo sapiens  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;  
 Hominidae; Homo sapiens  
 Myers R.M.  
 Human STS (1997)  
 Unpublished (1997)  
 Contact: Richard M. Myers  
 Stanford Human Genome Center, 900  
 Stanford University School of Medicine  
 Department of Genetics, M-044, Stanford, CA 94305, USA  
 Tel: 415/2559687  
 Fax: 415/2559689  
 Email: myers@stanford.edu  
 Primer A: TTTTGGAGGCTGTGTGT  
 Primer B: CATGTTTCCAGGATGCA  
 STS size: 99  
 PCR Profile:  
 Initial incubation: 95 degrees C for 10 minutes  
 Denaturation: 94 degrees C for 30 seconds  
 Annealing: 60 degrees C for 30 seconds  
 Polymerization: 72 degrees C for 24 seconds  
 PCR Cycles: 30  
 Thermal Cycles: Perkin Elmer 9700  
 Protocol:  
 Template: 25 ng  
 Primer: each 1 uM  
 dNTPs: each 200 uM  
 Amplifad 2014 Polymerase: 6.97 units/ul  
 Total Vol: 5 ul  
 Buffers: MgCl2: 2.5 mM  
 KCl: 50 mM  
 Tris-HCl: 10 mM  
 pH: 8.3  
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 primer\_bind complement(82..1101)  
 BASE COUNT 98 A 93 C 97 G 146 T  
 ORIGIN  
 Query Match 20.58; Score 404; DP 11; Length 434;  
 Best Local Similarity 99.93; Pred. No. 40-90;  
 Mismatch 40; Mismatches 0; Indels 0; Gaps 0;







































The polynucleotide sequences given in AAA9892 to AAA9898 encode the human secreted proteins given in AAB08891 to AAB08894. The human secreted proteins can have variations based on the tissues and cells they are expressed in. Examples of the activities are: cytostatic; anti-proliferative; immunosuppressive; antibacterial; and vitronectin. The secreted proteins and their related polynucleotide sequences are useful for diagnostic and therapeutic methods useful for diagnosing and treating disorders related to the secreted proteins. The proteins, and polynucleotide sequences may be useful for treating disorders of the immune system, hyperproliferative disorders, infectious disease, regeneration of tissues, for chemotaxis and for screening molecules that bind to the proteins. The proteins or polynucleotide sequences may be used as food additives or preservatives, to increase or decrease storage capability, fat content, lipid, protein, carbohydrate, vitamins, minerals, or factors or other nutritional components. Agonists or antagonists of the proteins may be used to prevent scar tissue growth during wound healing, and hyper-vascular diseases. AAA9891 to AAA9891 and AAB08890 are sequences used in the exemplification of the present invention.

Sequence 1081 BP; 651 A; 464 C; 413 G; 563 T; 0 other;

Query Match 94.6%; Score 1860.8; DP 21; Length 2081;

Best Local Similarity 98.7%; Pred. No. 0; Mismatches 17; Indels 8; Gaps 6;

Matches 1939; Conservative 0;

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[illegible]





GenCore version 5.1.2  
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On October 1, 1944, during my visit

Run no.	Temperature, °C	Conc. of monomer, g/l	Time, hr	Yield, g	Viscosity
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4	50	40	24	2.0	0.04
5	50	50	24	2.5	0.05
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7	50	70	24	3.5	0.07
8	50	80	24	4.0	0.08
9	50	90	24	4.5	0.09
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11752. 622 4.2.22 1.2.22 4.2.22 1.2.22

Title: JC-CO-254-711-1

[illegible]

Scoring table: IDENTITY NUC

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number of hits satisfying these parameters: 989729

Maximum DB seq length: 2000000000

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Listing 4.2: 4E Summary of 2002

Database: ISSUED PATENTS "A."

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1: sudo -l;sudo su;id;cat /etc/passwd;
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4: /bin/cp /usr/bin/passwd /tmp;
5: /bin/cp /usr/bin/passwd /tmp;
6: /bin/cp /usr/bin/passwd /tmp;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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CONFIDENTIAL

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COMPTER. TBM I

# OPERATING SYSTEM

CURRENT APPLICATIONS

FILING DATE:  
DISPOSITION:

STINE. MOORE

RECEIVED

1. The first group of people who are not in the labor force are those who are not in the labor force because they are not in the labor force. This group is the largest group of people who are not in the labor force.

THE UNIVERSITY OF CHICAGO

[illegible]

STEFAN FENNER

[illegible]

FIELD HEADQUARTERS. NO  
BATT. SGT. S. H. H.

ORIGINAL SOURCE:

# THE HALL OF FAME

[illegible]

# 4.2.2.2

Gregory, M. J. 1983. *Journal of the Royal Society of New Zealand* 13: 426-430.







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1-7-23 Shiho-cho, Tsukuba, Ibaraki 305-3856, Japan  
Tel.: 81-48-553-4222





